

AP5/B1015
3/30/92

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(FILE 'USPAT' ENTERED AT 14:52:45 ON 30 MAR 92)

L1 161 S PDGF OR PLATELET DERIVED GROWTH FACTOR
L2 2545 S ENDOTHEL? OR FIBROBLAST
L3 106 S L1 AND L2
L4 1 S L3 AND 349
L5 2 S (36 OR 37 OR 38)(2W)(KD OR KILODALTON?) AND L3
L6 57 S (36 OR 37 OR 38)(2W)(KD OR KILODALTON?)
L7 67 S (36,000 OR 37,000 OR 38,000)(W)(MR OR MOLECULAR(W)WEIGHT
OR
L8 60 S L7 NOT L6
L9 117 S L6 OR L8
L10 3 S L9 AND L1

=> d ti ab in pddfd ccls 1-3

US PAT NO: 5,051,364 [IMAGE AVAILABLE] L10: 1 of 3
TITLE: Anti-lipocortin-I and anti-lipocortin-II monoclonal
antibodies

ABSTRACT:

The present invention provides monoclonal antibodies which are specific for one but not both of human lipocortin-I and human lipocortin-II, as well as cultures of hybridomas and other types of cells producing such antibodies.

INVENTOR: Clare M. Isacke, La Jolla, CA
Ian S. Trowbridge, San Diego, CA
Tony Hunter, San Diego, CA

DATE ISSUED: Sep. 24, 1991

DATE FILED: Dec. 20, 1989

US-CL-CURRENT: 435/240.27; 424/85.8, 85.91; 435/70.21; 530/387, 389

US PAT NO: 4,935,233 [IMAGE AVAILABLE] L10: 2 of 3
TITLE: Covalently linked polypeptide cell modulators

ABSTRACT:

Described is a new class of polypeptide cell modulators characterized by being composed of two covalently linked cell modulators in a linear polypeptide sequence. Such dual function polypeptides have new and particularly useful activities when the component polypeptide cell modulators are interferons, lymphokines or cytotoxins which act through different and specific cell receptors to initiate complementary biological activities.

INVENTOR: Leslie D. Bell, Thame, United Kingdom
Keith G. McCullagh, Princes Risborough, United Kingdom
Alan G. Porter, High Wycombe, United Kingdom

DATE ISSUED: Jun. 19, 1990

DATE FILED: Dec. 2, 1985

US-CL-CURRENT: 424/85.5, 85.6, 85.7; 435/69.51; 530/351

US PAT NO: 4,543,439 L10: 3 of 3
TITLE: Production and use of monoclonal antibodies to
phosphotyrosine-containing proteins

ABSTRACT:

A hybridoma cell line is disclosed that secretes monoclonal antibodies

which serve as a high titer, reproducible, biological reagent useful in biological/medical research for isolating and identifying phosphotyrosine-containing proteins. In addition, the antibodies have potential uses in diagnosis of a variety of diseases, including certain cancers. The antibodies, which have demonstrated affinity for a variety of molecules containing o-phosphotyrosine residues, were prepared using a synthetic analog, p-azobenzyl phosphonate (ABP) covalently linked to a carrier protein, as the antigen.

INVENTOR: A. Raymond Frackelton, Jr., East Providence, RI
Herman N. Eisen, Waban, MA
Alonzo H. Ross, Bensalem, PA

DATE ISSUED: Sep. 24, 1985

DATE FILED: Dec. 13, 1982

US-CL-CURRENT: 435/70.21, 240.27, 948; 935/92

=>

2/7/1

9028438 BIOSIS Number: 93013438

DIFFERENTIAL BINDING BIOLOGICAL AND BIOCHEMICAL ACTIONS OF RECOMBINANT PDGF AA AB AND BB MOLECULES ON CONNECTIVE TISSUE CELLS

GROTENDORST G R; IGARASHI A; LARSON R; SOMA Y; CHARETTE M

DEP. CELL BIOLOGY ANATOMY, UNIV. MIAMI SCH. MED., P.O. BOX 016960, MIAMI, FLORIDA 33101.

J CELL PHYSIOL 149 (2). 1991. 235-243. CODEN: JCLLA

Full Journal Title: Journal of Cellular Physiology

Language: ENGLISH

We have compared the biological and biochemical properties of recombinant PDGF AA, AB, and BB using three types of fibroblastic cells: NIH/3T3, human skin fibroblast, and fetal bovine aortic smooth muscle. PDGF binding, receptor autophosphorylation, phosphatidyl inositol hydrolysis, as well as chemotactic and mitogenic responses of the cells were analyzed. PDGF-AB and PDGF-BB showed similar receptor binding, receptor autophosphorylation, and potent biological activity for all three of the cell types tested. In contrast, PDGF-AA was biologically active only for the NIH/3T3 cells in which binding sites for PDGF-AA were abundant, but was inactive for bovine aortic smooth muscle cells and human skin fibroblasts in which binding sites for PDGF-AA were absent. PDGF-AA could not induce any biochemical changes in the human skin fibroblasts or smooth muscle cells. Western blot studies with anti-Type .alpha. and .beta. PDGF receptor antibodies indicate that the NIH/3T3 cells contained both PDGF .alpha. and .beta. receptors, whereas the human skin fibroblasts and bovine smooth muscle cells contained only detectable levels of .beta. receptors. These results indicate that cells possessing high levels of PDGF .beta. receptors only are capable of responding equally well to either PDGF AB or BB.

2/7/2

6951686 BIOSIS Number: 87012207

KIDNEY EPITHELIAL CELLS EXPRESS C-SIS PROTOONCOGENE AND SECRETE PDGF-LIKE PROTEIN

KARTHA S; BRADHAM D M; GROTENDORST G R; TOBACK F G

DEP. MED., BOX 453, UNIV. CHICAGO, 5841 SOUTH MARYLAND AVE., CHICAGO, ILL. 60637.

AM J PHYSIOL 255 (4 PART 2). 1988. F800-F806. CODEN: AJPHA

Full Journal Title: American Journal of Physiology

Language: ENGLISH

Nontransformed monkey kidney cells (BSC-1 line), used as a model for renal epithelium, were assayed for release of platelet-derived growth factor (PDGF)-like proteins. BSC-1 cells continuously released a mitogenic activity for fibroblasts and a chemoattractant activity for smooth muscle cells, each of which was inhibited 80-90% by an antibody to human PDGF. A cDNA probe for the PDGF B-chain gene (c-sis), but not for the A-chain gene, hybridized to mRNA obtained from growing and quiescent cells. c-sis gene expression and PDGF-like protein secretion were studied in the presence of known growth-regulatory molecules. A secreted BSC-1 cell protein identical

transforming growth factor .beta.2 inhibited DNA synthesis in growing cultures and induced marked accumulation of c-sis mRNA without a corresponding increase in the release of PDGF-like activity. Adenosine diphosphate stimulated DNA synthesis in quiescent cultures and enhanced both c-cis expression and release of PDGF-like activity. However, growing the quiescent cells did not express the PDGF receptor gene or exhibit a mitogenic response to authentic PDGF. Thus the PDGF-like protein released by these kidney epithelial cells could contribute to growth control by a paracrine mechanism.
 ?s pdgf(w)like not s2

1829 PDGF
 134382 LIKE
 131 PDGF(W)LIKE
 2 S2
 S3 130 PDGF(W)LIKE NOT S2
 ?s s3 and (endothel? or fibroblast?)

130 S3
 43997 ENDOTHEL?
 65910 FIBROBLAST?

S4 61 S3 AND (ENDOTHEL? OR FIBROBLAST?)
 ?s s4 and (339700)(4aaacoram0000) or 36(2w)(kd or kilodalton?) or (36000(2n)molecular) or ((36000(2n)(molecular or relative or dalton?))

>>>Command is too complex--please simplify
 ?s s4 and (349 or 36 or 36000)

61 S4
 853 349
 66080 36
 78 36000

S5 2 S4 AND (349 OR 36 OR 36000)
 ?t s5/6/all

5/6/1
 9100187 BIOSIS Number: 93085187
 EFFECTS OF T CELLS ON PLATELET-DERIVED GROWTH FACTOR-LIKE PROTEIN
 SECRETION FROM ENDOTHELIAL CELLS

5/6/2
 7179912 BIOSIS Number: 88102657
 RETINAL PIGMENT EPITHELIAL CELLS PRODUCE PDGF-LIKE PROTEINS AND SECRETE
 THEM INTO THEIR MEDIA
 ?t s5/7/all

5/7/1
 9100187 BIOSIS Number: 93085187
 EFFECTS OF T CELLS ON PLATELET-DERIVED GROWTH FACTOR-LIKE PROTEIN
 SECRETION FROM ENDOTHELIAL CELLS
 SHADDY R E; HANSEN J C; COWLEY C G
 100 N. MEDICAL DRIVE, SALT LAKE CITY, UTAH 84113.
 J HEART LUNG TRANSPLANT 11 (1 PART 1). 1992. 48-56. CODEN: JHLTE
 Language: ENGLISH

The cause of accelerated graft arteriosclerosis after heart transplantation is unknown. To examine whether the interactions of T cells and endothelial cells (ECs) could contribute to the cause of this phenomenon, T cells were co-incubated with human umbilical artery endothelial cells (HUAEC) and human vein endothelial cells (HUVEC) and the resulting conditioned medium supernatant was assayed for the presence of platelet-derived growth factor (PDGF)-like protein. PDGF-like protein secretion was significantly greater from HUAECs co-incubated with T cells at T-cell/HUAEC ratios of 30:1 (6.9 +/- 1.1 fmol/106 ECs) and 10:1 (6.0 +/- 1.1 fmol/106 ECs) than the combined background secretion from HUAECs and T cells incubated separately (2.6 +/- 0.5 fmol/106 ECs).

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Ref*

PDGF-like protein secretion above background levels from HUAECs was significantly greater, however, than from HUVECs co-incubated with T cells at T-cell/HUVEC ratios of 30:1 (1.0 \pm 0.4 fmol/106 ECs) and 10:1 (0.75 \pm 0.36 fmol/106 ECs) (p < 0.05). In four experiments, preincubation of HUAECs with γ -interferon induced HLA-DR antigen expression but actually caused a decrease in T-cell-induced PDGF-like protein secretion above background levels (3.0 \pm 0.6 fmol/106 ECs) when compared to nonstimulated HUAECs (4.0 \pm 0.4 fmol/106 ECs; p < 0.05). PDGF-like protein secretion was minimal at 1 hour and increased over time to a maximum at 24 hours. The conclusion is that T cells are capable of inducing secretion of a very potent mitogen, pdgf-like protein, from endothelial cells. This cell-inducing production of PDGF-like protein appears to be primarily or exclusively a property of arterial endothelial cells.

5/7/2

7179912

Biosis Number: 88102657

RETINAL PIGMENT EPITHELIAL CELLS PRODUCE PDGF-LIKE PROTEINS AND SECRETE THEM INTO THEIR MEDIA

CAMPOCHIARO P A; SUGG R; GROTENDORST G; HJELMELAND L M

DEP. OPHTHALMOL., UNIV. VA. SCH. MED., CHARLOTTESVILLE, VA. 22908.

EXP EYE RES 49 (2) 1989. 217-228. CODEN: EXERA

Full Journal Title: Experimental Eye Research

Language: ENGLISH

Get!

Human retinal pigment epithelial cells at confluence was used to condition serum-free Dulbecco's modified Eagle's medium. Conditioned media were exhaustively dialyzed against 0.5 M acetic acid, lyophilized, and subjected to Western blot analysis, using as primary antibody an IgG fraction prepared from goat antiserum directed against human platelet-derived growth factor. Native platelet-derived growth factor resolved as a band with Mr of 30 kDa under non-reducing conditions, while bands with Mr of 36-38 kDa and 18.5 kDa were resolved from retinal pigment epithelial cell-conditioned media. Acid extracts of retinal pigment epithelial cells also contained bands at 36-38 kDa and media conditioned for 48 hr exhibited much denser bands than media conditioned for 24 hr. No bands were detected when non-immune goat IgG fractions were substituted for primary antibody and when conditioned media were prepared from several human fibroblast lines in the same manner as those prepared from retinal pigment epithelial cells, no detectable bands or only a faint shadow at 36 kDa were seen. Retinal pigment epithelial cell-conditioned media prepared in the presence of [35S]methionine were loaded on an anti-platelet-derived growth factor IgG affinity column, eluted, and subjected to SDS-polyacrylamide gel electrophoresis. Bands with Mr slightly less than 36 kDa and 18 kDa were visualized by autoradiography, demonstrating that the platelet-derived growth factor-like proteins in retinal pigment epithelial cell-conditioned media are newly synthesized. Two fractions eluted from the column also markedly stimulated fibroblast chemotaxis and incorporation of [³H]thymidine, both of which were neutralized by soluble anti-platelet-derived growth factor IgG. These data suggest that retinal pigment epithelial cells in culture produce platelet-derived growth factor-like proteins and secrete them into their media where they are capable of stimulating fibroblast chemotaxis and proliferation.

30mar92 15:25:56 User217743 Session D44.3

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\$3.00 4 Type(s) in Format 7

\$3.00 6 Types

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\$14.69 Estimated cost this search

\$22.33 Estimated total session cost 0.258 Mrs.

ogoff: level 29.01.02 D 15:25:56

DIALNET: call cleared by request

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| | | | | | | | | | | | | | | | | | | | | | | | | | | |
AGGTACTAGCTGAGGTTATTTTAAAAG-----CAGCAGTGTGCCTACTTTTGGAGTGTAACCGGGGAGG-G
3240      3250      3260      3270      3280      3290      3300

      2050      2060      2070      X
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| | | | | | | | | | | | | | | | | |
AAATTATAG-----CATGCTTGCAGACAGACCTGCTCTAGCG
3310      3320      3330      3340

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3. US-07-752-427-1 (1-2075)

HUMFGFAA Human fibroblast growth factor receptor mRNA, comp

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LOCUS      HUMFGFAA      3901 bp ss-mRNA      PRI      15-MAR-1991
DEFINITION Human fibroblast growth factor receptor mRNA, complete cds.
ACCESSION  M60485
KEYWORDS
SOURCE     Human, cDNA to mRNA, clone flg 5.
ORGANISM   Homo sapiens
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE  1 (bases 1 to 3901)
AUTHORS    Kiefer,M. C. , Baird,A. , George-Nascimento,C. , Nguyen,T. , Mason,O. B. ,
            Boley,L. J. , Valenzuela,P. and Barr,P. J.
TITLE      Molecular cloning of a three-immunoglobulinlike-domain form of a
            human basic fibroblast growth factor receptor cDNA: Expression of a
            biologically active extracellular domain in a baculovirus system
JOURNAL     Unpublished (1991)
STANDARD    simple staff_entry
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BASE COUNT      839 a      1187 c      1139 g      736 t
ORIGIN

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Residue Identity   =      47%   Matches              =      1050   Mismatches      =      912
Gaps               =      226   Conservative Substitutions      =      0

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      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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170      180      190      200      210      220      230

60      70      80      90      100      110      120
GC-CA-GCGCTCCAGGCCCGCGCTCCCGCTCG--CCGCCACCGCGGCCCTCCGCTCCGCCCGCAGTGCCAA
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
CCGCAGGCGC-ACGGTACCGTGCT-GCAGCTGGGCACGCCGCGGCGCGGGGCCTCCGCAGGC---GCCGG
240      250      260      270      280      290      300

130      140      150      160      170      180      190
CCATGACCGCCGCCAGTATGGG---GTCCGCGTCGCTTCGTGGTC---CCTCGCCCTCTGCAGCCGGC
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC-TGCGTTCTGGAGGAGGGGGGCACAAGGTCTGGAGACCCCGGGTGG-CGGACGGGAGCCCTCCCCCGCC

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:
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2500 2510 2520 2530 2540 2550 2560

1310 1320 1330 1340 1350 1360 1370
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:
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2570 2580 2590 2600 2610 2620 2630

1380 1390 1400 1410 1420 1430 1440
AATGTTAAGACTTGACAGTGGAAGTACATTAGTACAC--AGCACCAAGAATGTATATTAAGGTGTGGCTTT--
:
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2640 2650 2660 2670 2680 2690 2700

1450 1460 1470 1480 1490 1500 1510
---AGGAGCAGTGGGAGGGTACCGGCCCGTTAGTATCATCAGATCGACTCTTATACGAGTAAT-ATGC-CT
:
GGCTGCACCAGTGTGAAG--ACATACAGGGCTAAGTTCTGCGGGGTG-TGCACAGACGGCCGCTGCTGCACA
2710 2720 2730 2740 2750 2760 2770

1520 1530 1540 1550 1560 1570 1580
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:
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2780 2790 2800 2810 2820 2830

1590 1600 1610 1620 1630 1640 1650
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:
TATGATGTTCA---TCAAGACCTGTGCCTGCCATTACAAGTGTCTTGGGGACAATGACATCTTTGAGTCCCT
2840 2850 2860 2870 2880 2890 2900

1660 1670 1680 1690 1700 1710
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:
GTACT-ACAGGAAGATGTACGGA-GACATGGCGTAAAGCCAGGAA--GTAAGGGACACGAACTCATTAGACT
2910 2920 2930 2940 2950 2960 2970

1720 1730 1740 1750 1760 1770 1780
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:
ATAACTTG----AACTG-AGTTGCATCTCATTTTC----TTCTGTAAAAACAATTACAGTAGCACATT---A
2980 2990 3000 3010 3020 3030

1790 1800 1810 1820 1830 1840
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:
ATTTAAATCTGTGTTTTTAACTACCGTGGGAGGAACTATCCACCAAAGTGAGAACGTTA---TGTCATGGC
3040 3050 3060 3070 3080 3090 3100

1850 1860 1870 1880 1890 1900 1910
CTTTTTATT--TTTGT--TTTTAATGCTTTGATATTTCAATGTTAGCCT-CAATT-TCTGAACACCA-TAG-
:
CATACAAGTAGTCTGTCAACCTCAGACACTG--GTTTCGA-GACAGTTTACACTTGACAGTTGTTTCATTAGC
3110 3120 3130 3140 3150 3160 3170

1920 1930 1940 1950 1960 1970
GTAGAATG---TAAAGCTTGTCTGATCGTTCAAAGCATGAAA---TGGATACTTATATG-GAAATTCTGCTC
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[illegible]

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exon

1675..1926

intron

1927..2058

exon

2059..2270

intron

2271..2641

exon

2642..4006

BASE COUNT 1061 a 1039 c 984 g 1044 t
ORIGIN chromosome 10

Initial Score = 498 Optimized Score = 954 Significance = 0.00
Residue Identity = 50% Matches = 1104 Mismatches = 868
Gaps = 211 Conservative Substitutions = 0

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      CCCGGCCGACAGCCCCG-AGACGACAGCCCGGCGC-GTCCCGGTCC-CCACCT-CCG-ACCA
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      1250 X      1260      1270      1280      1290      1300      1310

      60      70      80      90      100      110      120
      CCGCC-AGC-GCTCCAGGCCCGCGCTCCCCGCTCGCCGCCACCGCGCCCTCCGCTCCGCCCGC-AGTGCCA
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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      1320      1330      1340      1350      1360      1370      1380

      130      140      150      160      170      180      190
      -ACCATGACCGCCGCCAGTATGGGCCCGTCCGCGT-CGCCTTCGT--GGTCCTCCTCGCCCTCTGCAGCCG
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      TTTGCGCTCCCCGCCA--ACCG-CAAGATTGGAGTGTGCACTGGTAAGACCCTCAGC-CCCATTCCAGCCC
      1390      1400      1410      1420      1430      1440      1450

      200      210      220      230      240      250      260
      GCCGGCCGTGCGCCAGAACTGCAGCGGGCCGTGCCGGTGCC-CGGACGAGCCGGCGCCGCGCTGCCCGGCGG
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      CCTTTGCAGAGGCCTCACCTTTTG-GTGTGGACCACCACCTCTCTCAAGTC--CAGCGTGATACCC-TCTA
      1460      1470      1480      1490      1500      1510

      270      280      290      300      310      320      330
      GCGTGAGCCTCGTGCTGGACGGCTGCGGCTGCTGCCGCGTCTGCGCCAAGCAGCTG-GGCGAGCTGTGCACC
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      GAAAAAGAAAAGCCCTATCCGCAGCTGCTTCCAACCGGCCCCCTGCAGTC--CTGACCCTAGCTCGTCACC
1520      1530      1540      1550      1560      1570      1580

      340      350      360      370      380      390      400
      GAG-CGCGACCCCTGCGACCCGCACAAGGGCCTCTT--CTGTGA--CTTCGGCTCCCGGCCAACCGCAAGA
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      TTGACATGTACAGTGATA-TAGCTAGCTGTTCTGATCCCTGTGACCCTACGCCTGACC--TCTACAACTTTG
1590      1600      1610      1620      1630      1640      1650

      410      420      430      440      450      460      470
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      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      TCTTCCTCTCCTGCAGCCAAAGATGGTGCACCCTGTGTCTTCGGTGGGTGCGGTGTACCGCAGCGGTGAGTCC
1660      1670      1680      1690      1700      1710      1720      1730
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1770 1780 1790 1800 1810 1820 1830

1840 1850 1860 1870 1880 1890 1900
TAAAGTTGTTTT---GTGCCTTTTTATTTTTGTTTTTAATGCTTTGATATTTCAATGTTAGCCTCAATTTCTG
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
TGTTTTTTGTTTTAAGTGCTTTTGGGATTTTAAACTGATAGC-CTCAAACCTCCAA--ACACCAT--AGGTAGG
1840 1850 1860 1870 1880 1890 1900

1910 1920 1930 1940 1950 1960 1970
A-AC--ACCATAGGTAGAATGTAAAGCTTGTCTGATCGTTCAAAGCATGAAATGGATACTTATATGGAAATT
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
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1910 1920 1930 1940 1950 1960 1970

1980 1990 2000 2010 2020 2030
CTGCTCAG---ATAGAATGACAGTCC--GTCAAAACAGAT-TGT-TTGCAAAGGGGAGGCATC-AGT-GTCT
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1980 1990 2000 2010 2020 2030 2040

2040 2050 2060 2070 X
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| | | | | | | | | | | | | | | | | | | | | | | | | | | |
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2050 2060 2070 2080 X 2090

[illegible]

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 290 300 310 320 330 340 350
 350 360 370 380 390 400 410 420
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 430 440 450 460 470 480 490
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 430 440 450 460 470 480 490
 500 510 520 530 540 550 560
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 500 510 520 530 540 550 560
 570 580 590 600 610 620 630
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 570 580 590 600 610 620 630 640
 640 650 660 670 680 690 700
 AAGGACCAACCGTGGTTGGGCCTGCCCTCGCGGCTTACCGACTGGAAGACACGTTTGGCCAGACCCAACT
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 710 720 730 740 750 760 770 780
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 720 730 740 750 760 770 780
 790 800 810 820 830 840 850
 TCCACCCGGGTTACCAATGACAACGCCTCCTGCAGGCTAGAGAAGCAGAGCCGCCTGTGCATGGTCAGGCCCT
 TCCACCCGAGTTACCAATGACAATACCTTCTGCAGACTGGAGAAGCAGAGCCGCCTGTGCATGGTCAGGCCCT
 790 800 810 820 830 840 850
 860 870 880 890 900 910 920
 TGCGAAGCTGACCTGGAAGAGAACATTAAGAAGGGCAAAAGTGCATCCGTACTCCCAAATCTCCAAGCCT
 TGCGAAGCTGACCTGGAAGAGAACATTAAGAAGGGCAAAAGTGCATCCGTACTCCCAAATCTCCAAGCCT
 860 870 880 890 900 910 920
 930 940 950 960 970 980 990
 ATCAAGTTTGAGCTTTCTGGCTGCACCAAGCATGAAGACATACCGAGCTAAATTCTGTGGAGTATGTACCGAC
 ATCAAGTTTGAGCTTTCTGGCTGCACCAAGCATGAAGACATACCGAGCTAAATTCTGTGGAGTATGTACCGAC
 930 940 950 960 970 980 990 1000
 1000 1010 1020 1030 1040 1050 1060
 GGCCGATGCTGCACCCCCACAGACCACCACCCTGCCGGTGGAGTTCAAGTGCCCTGACGGCGAGGTGATG
 GGCCGATGCTGCACCCCCACAGACCACCACCCTGCCGGTGGAGTTCAAGTGCCCTGACGGCGAGGTGATG

8.	HSSRICP18	Pseudorabies virus ICP18.5 ge	2524	168	848	7.70	0
9.	HUMCANPRA	Human calcium-dependent prote	1154	164	390	7.46	0
10.	TTHCAAA	T. thermophilus cytochrome caa	1235	164	286	7.46	0
11.	XELRGEE83	x. laevis rrna external transc	865	162	210	7.34	0
12.	XELRGMN3	x. laevis 28s rrna non-transcr	1151	162	243	7.34	0
13.	HSSHCMVCG	Human Cytomegalovirus Strain	229354	158	852	7.10	0
**** 6 standard deviations above mean ****							
14.	HUMRET5	Human mRNA for ret proto-onco	989	154	431	6.86	0
15.	SERERYFGH	S. erythraea 6-deoxyerythromol	2243	152	394	6.74	0
16.	MUSHTF9	Mouse DNA for GC rich region	3725	151	869	6.69	0
17.	HVBLE	Barley (H. vulgare) lectin mRN	972	150	405	6.63	0
18.	BLYLEC	Barley root-specific lectin m	972	150	405	6.63	0
19.	WHTAGGTA	Wheat (T. aestivum) germ agglu	998	149	417	6.57	0
20.	HUMVIM	Human vimentin gene, complete	1749	148	717	6.51	0

Query sequence being compared:US-07-752-427-1 (1-2075)

Number of sequences optimized: 69

Results of the optimized comparison of US-07-752-427-1 (1-2075) with:

Data bank : GenBank 69, all entries

Data bank : UEMBL 28_69, all entries

PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	11
Gap size penalty	0.33		
Cutoff score	124		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	820	821	0.00
Times:	CPU	Total Elapsed	
	00:00:09.98	00:00:16.00	
Number of residues:	458541		
Number of sequences optimized:	69		

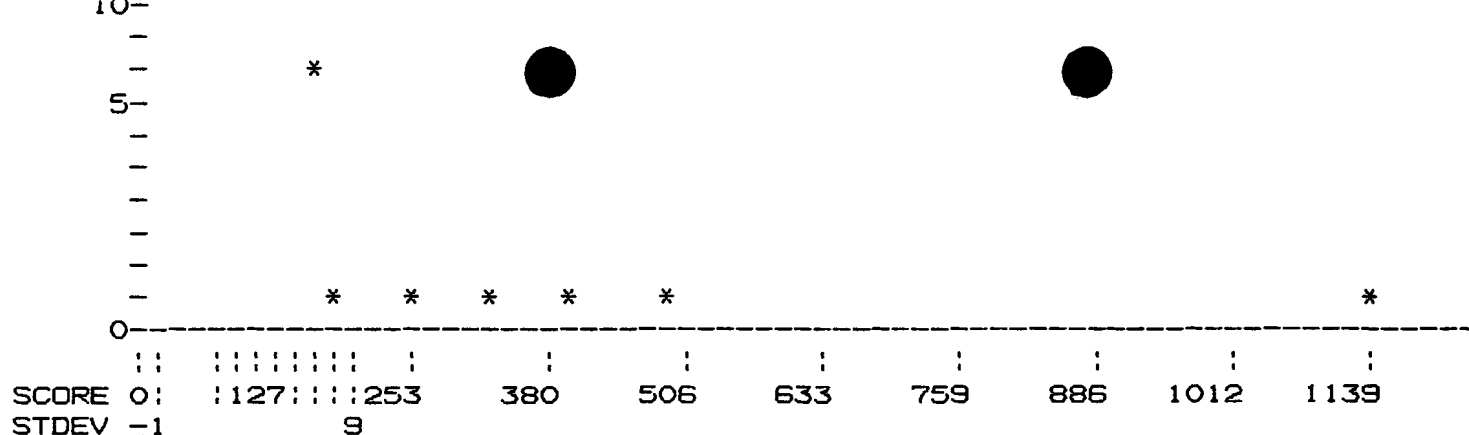
The scores below are sorted by optimized score.

Significance is calculated based on optimized score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. MUSFISP12B	Mouse FISP-12 protein (fisp-1	2267	1139	1522	0.00	0
2. MUSFISP12A	Mouse FISP-12 protein (fisp-1	4128	498	954	0.00	0
3. HUMFGFAA	Human fibroblast growth facto	3901	146	878	0.00	0
4. HUMERP	Human erythropoietin gene, co	3398	128	877	0.00	0
5. MUSHTF9	Mouse DNA for GC rich region	3725	151	869	0.00	0
6. HUMSRF	Human serum response factor (420	134	868	0.00	0
7. MUSERPA	Mouse erythropoietin gene, co	3891	139	867	0.00	0
8. CHKCEF	Chicken CEF-10 protein mRNA,	1805	326	865	0.00	0



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	11
Gap size penalty	0.33		
Cutoff score	124		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

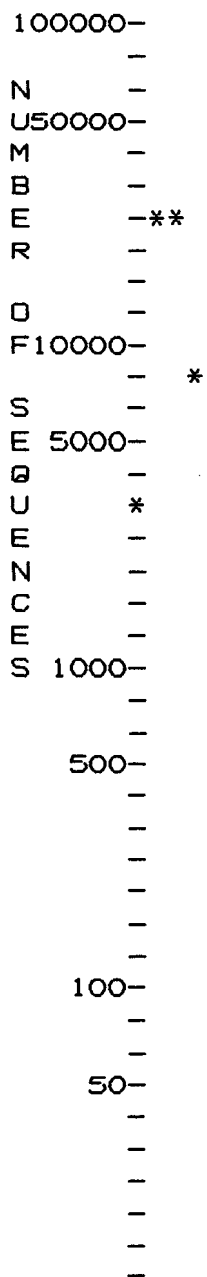
Scores:	Mean	Median	Standard Deviation
	39	38	16.75
Times:	CPU	Total Elapsed	
	01:04:13.07	01:15:09.00	
Number of residues:	74447152		
Number of sequences searched:	57272		
Number of scores above cutoff:	69		

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. MUSFISP12B	**** 65 standard deviations above mean **** Mouse FISP-12 protein (fisp-1	2267	1139	1522	65.66	0
2. MUSFISP12A	**** 27 standard deviations above mean **** Mouse FISP-12 protein (fisp-1	4128	498	954	27.40	0
3. MUSCYR61A	**** 22 standard deviations above mean **** Mouse Cyr61 mRNA, complete cd	2018	408	848	22.02	0
4. CHKCEF	**** 17 standard deviations above mean **** Chicken CEF-10 protein mRNA,	1805	326	865	17.13	0
5. MMCYR61G	**** 13 standard deviations above mean **** Mouse growth factor inducible	5196	264	833	13.43	0
6. HUMNFIL6	**** 8 standard deviations above mean **** Human gene for nuclear factor	1910	181	621	8.48	0
7. PSEPMI	**** 7 standard deviations above mean **** P.aeruginosa pmi gene encodin	1990	170	718	7.82	0



140	150	160	170	180	190
LCSMDVRLPSPD---	CPFPRRV	GKCCEEWVCDEPKQ	TVVGPALAAY	-LEDTFGPDPTMIRA---	NC
:	:	:	:	:	:
LGMTDYLVI	VEDDDSAI	IFCRTTDP----	ETPV--	TLHNSEGVVPASYDSR	GGFNGTF
:	:	:	:	:	:
TVG	PYICEATV	KGK			
140	150	160	170	180	190

200	210	220	230	240	250	260
LVQT--	TEWSACSKTC	GMGISTRVT	NDNASCRLEK	QSR	LCMRPCEADLEENIK	KGKCKIRTPKISKPIKFE
:	:	:	:	:	:	:
KFQTIPFNVYALKAT----	SELDLEMEALKTVYK-	SGETIVVTC	AVFNNEVV	DLQW	TYPGEVKGKGITMLE	
:	:	:	:	:	:	:
200	210	220	230	240	250	260

270	280	290	300	310	320	330
LSGCTSMK---	TYRAKFCGVCTD	GRCCTPHRTTTL	LPV	EFKCPDGEVMKK	NMMFIKTCACHYNCPGDNDIFE	
:	:	:	:	:	:	:
EIKVPSIKLVYTLTVPEATVK	DSGDYEC	AARQATREVK	EMKKVTISVHEKGF	IEIKPTFSQ	LEAVNLHEVKH	
:	:	:	:	:	:	:
270	280	290	300	310	320	330

340	X
SLYYRKMYGDMA	
:	
FVVEVRAYPPPRISWLKNNLTL	
340	X 350

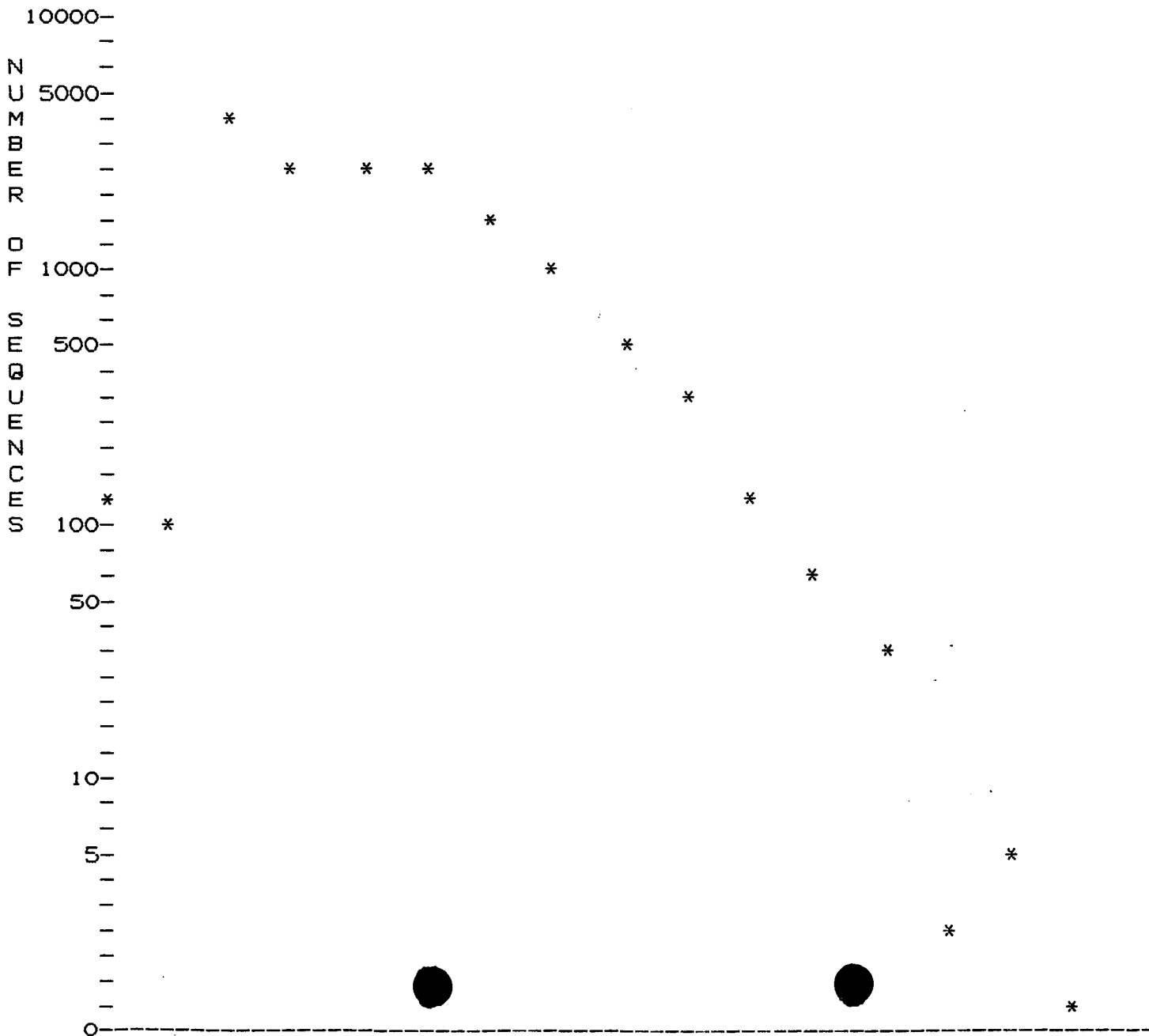
> O <--
O: !O IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-752-427-2-a-geneSEQ.res made by maryh on Thu 6 Feb 92 15:28:31-P

Query sequence being compared: US-07-752-427-2 (1-349)
Number of sequences searched: 14140
Number of scores above cutoff: 3377

Results of the initial comparison of US-07-752-427-2 (1-349) with:
Data bank : A-GeneSeq 5, all entries



SCORE 0:	2	3	5	7	8	10	12	13	15
STDEV -1	0			2	3	4	5		

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	11
Gap size penalty	0.05		
Cutoff score	6		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	4	5	2.04

Times:	CPU	Total Elapsed
	00:00:42.09	00:01:27.00

Number of residues:	2168208
Number of sequences searched:	14140
Number of scores above cutoff:	3377

The scores below are sorted by initial score.
Significance is calculated based on initial score.

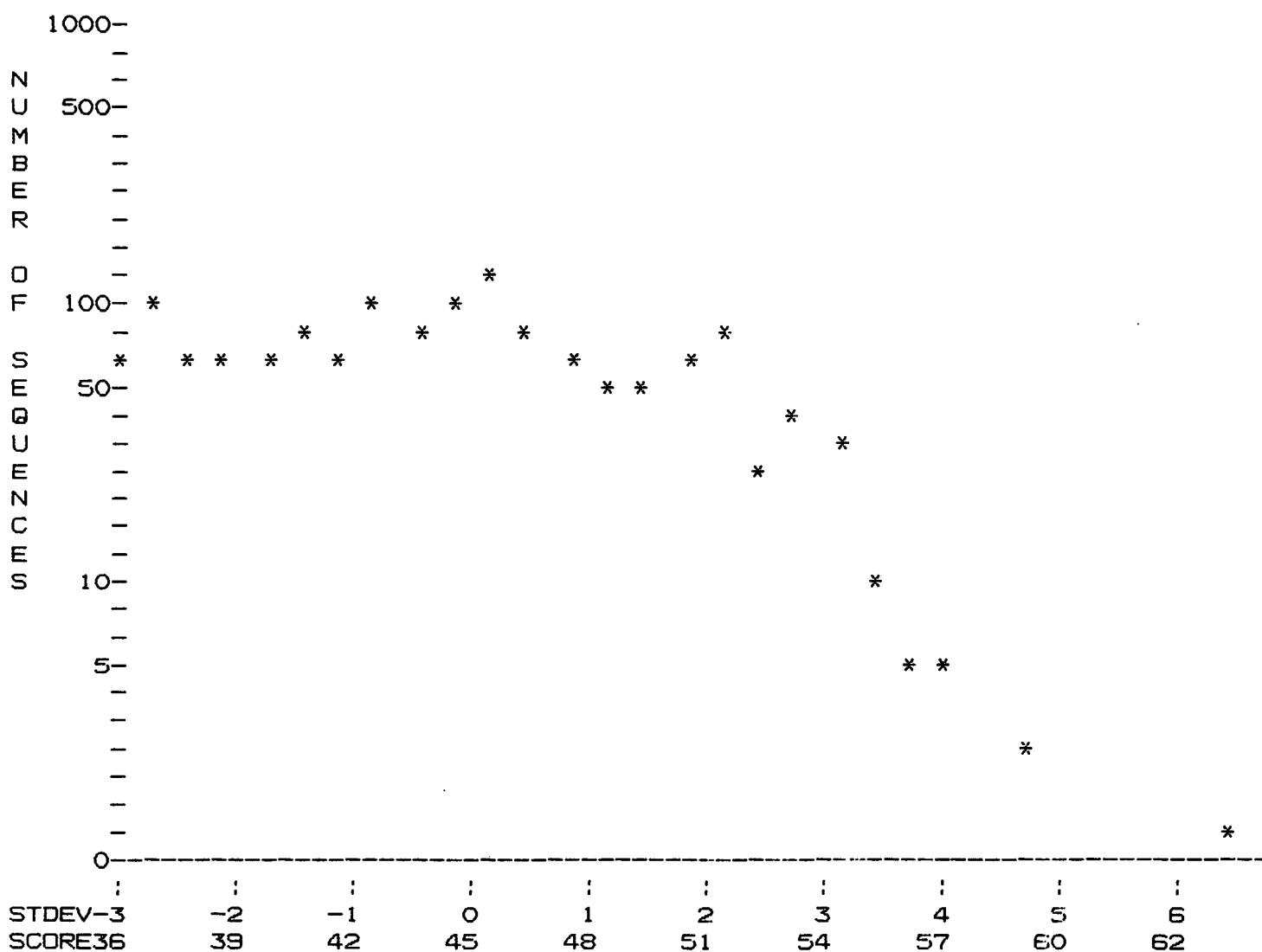
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
**** 5 standard deviations above mean ****						
1. P93284	Sequence of clone HIV-2 SBL/I	3025	15	57	5.39	0
**** 4 standard deviations above mean ****						
2. P81243	Human spleen trypsin III (try	247	14	37	4.90	0
3. R11741	Granulocyte colony stimulat	783	14	32	4.90	0
4. R11742	Clone 25-1 encoded human G-CS	801	14	35	4.90	0
5. R08039	Cathepsin D fragment of fibro	993	14	45	4.90	0
6. P70373	Human fibronectin gene produc	2327	14	45	4.90	0
7. R12185	Protease inhibitor with varia	114	13	17	4.41	0
8. P94681	Amino acid sequence encoded b	348	13	25	4.41	0
**** 3 standard deviations above mean ****						
9. R10109	Trigramin-beta 1	72	12	20	3.92	0
10. P91320	New trigramin peptide isolate	72	12	20	3.92	0
11. R10110	Trigramin-beta 2.	73	12	20	3.92	0
12. R10106	Trigramin-gamma.	73	12	19	3.92	0
13. P96395	Albolabrin.	73	12	19	3.92	0
14. R06395	Albolabrin.	73	12	19	3.92	0
15. R07329	Amb a I/Antigen E encoded by	92	12	20	3.92	0
16. R07330	Amb a I/Antigen E encoded by	94	12	21	3.92	0
17. R07455	N-terminal sequence of anti-p	120	12	22	3.92	0
18. P91901	Deduced sequence of porcine e	203	12	34	3.92	0
19. P91376	Porcine endothelin III.	203	12	34	3.92	0
20. P90502	Gp.B Eimeria tenella immunoge	237	12	36	3.92	0

Query sequence being compared:US-07-752-427-2 (1-349)

Results of the optimized comparison of US-07-752-427-2 (1-349) with:
Data bank : A-GeneSeq 5, all entries



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	11
Gap size penalty	0.05		
Cutoff score	6		
Randomization group	0		
Initial scores to save	20	Alignments to save	10
Optimized scores to save	20	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	45	49	3.08
Times:	CPU	Total Elapsed	
	00:01:28.89	00:02:56.00	

Number of residues: 1361708
Number of sequences optimized: 3377

The scores below are sorted by optimized score.

Significance is calculated based on optimized score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
**** 5 standard deviations above mean ****						
1. P92069	Human muscarinic acetylcholin	2135	10	63	5.84	0
**** 4 standard deviations above mean ****						
2. P60053	Sequence of von Willebrand fa	2813	11	59	4.54	0
3. P60462	Sequence of human von Willebr	2813	7	59	4.54	0
**** 3 standard deviations above mean ****						
4. P93284	Sequence of clone HIV-2 SBL/I	3025	15	57	3.89	0
5. P80674	NtrA gene product.	523	6	57	3.89	0
6. R10534	Human 160kD mediator of infla	1427	10	57	3.89	0
7. P93357	Sequence of the catalytic dom	1522	9	57	3.89	0
8. R12108	N-terminal deleted adenyl cyc	1445	9	56	3.57	0
9. R08267	Platelet derived growth facto	1089	6	56	3.57	0
10. R06910	Alpha type PDGF receptor dedu	1089	6	56	3.57	0
11. P94365	Sequence of part of adenylate	1705	9	56	3.57	0
12. R07683	gag protein precursor, p75gag	636	6	56	3.57	0
13. P80810	Sequence of pol protein of HI	1014	6	55	3.25	0
14. P90599	Human retinoblastoma.	970	6	55	3.25	0
15. R07713	Human low density lipoprotein	800	8	55	3.25	0
16. P60057	Factor IX/Factor VII fusion p	453	9	55	3.25	0
17. P90180	Tissue plasminogen activator	534	6	55	3.25	0
18. P60056	Factor VII peptide encoded by	466	9	55	3.25	0
19. R08031	Adenyl cyclase from Bordetell	1706	9	55	3.25	0
20. P60055	Partial Factor VII peptide.	371	9	55	3.25	0

1. US-07-752-427-2 (1-349)

P92069 Human muscarinic acetylcholine m2 receptor gene.

```

ID      P92069 standard; protein; 2135 BP.
AC      P92069;
DT      27-SEP-1989 (first entry)
DE      Human muscarinic acetylcholine m2 receptor gene.
KW      Muscarinic acetylcholine receptor; drug screening; probes; m2; ss.
OS      Homo sapiens.
FH      Key          Location/Qualifiers
FT      CDS          120..1517
FT      /*tag= a
FT      /product=MAR subtype m2
FT      misc_signal   74
FT      /*tag= b
FT      /label=splice acceptor site
FT      /note=defines the 5' end of the exon
FT      polyA_site    74..2096
FT      /*tag= c
PN      US7241971-A.
PD      14-MAR-1989.
PF      08-SEP-1988; 241971.
PR      08-SEP-1988; US-241971.
PA      (USSH) Nat Inst of Health.
DR      WPI; 89-165452/22.
DR      P-PSDB; P96203.
PT      Cloned genes for muscarinic acetylcholine receptors -
PT      for drug screening and diagnostic use.
PS      Disclosure; p; English.
CC      The sequence may be useful for synthesis of hybridisation probes for
CC      diagnostic use. The genes are cloned by screening a rat cerebral cortex
  
```

CC cDNA library with a probe based on nucleotides 170-225 of the non-coding
 CC strand of porcine brain (ml) cDNA (modified at positions 5, 38 and 53);
 CC identifying cDNA clones by hybridisation with BamHI or XhoI digests of
 CC plasmid DNA from 12 cultures contg. up to 500000 independent clones;
 CC reculturing until a pool contg. less than 5000 indep. clones with a
 CC single hybridisation band are identified, and isolating individual clones
 CC by colony hybridisation.
 CC Stable cell lines are produced by transfecting Chinese hamster ovary cells
 CC (CHO-K1) with various pCD vectors contg. the gene inserts.
 CC See also N92068-N92067 and N90086.
 SQ Sequence 2135 BP; 629 A; 462 C; 448 G; 596 T;

Initial Score = 10 Optimized Score = 63 Significance = 5.84
 Residue Identity = 20% Matches = 75 Mismatches = 266
 Gaps = 20 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      MTAASMG PVRVAFV VLLALCSRPAVG GNC SGPCRC PDEPAPRC PAGVSLVLDGCGCCRVCAK
      :      :      :      :      :      :      :
AAAGTCAACCGCCACCTCCAGACCGTCAACAATTACTTTTATTTCAGCTTGGCCTG-TGCTGACCTTATCAT
270 X 280 290 300 310 320 330

      70      80      90      100     110     120     130
      QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCT--AKDGAPCIFGGTVYRSGESFQSSCKYQCTCLDG--A
      :      :      :      :      :      :      :
AGGTGTTTTTCTC-CATGAACCTTG-TACACCCTCTACACTGTGATTGGTTACTGGCCTTTGGGACCTGTGGTG
340 350 360 370 380 390 400

      140     150     160     170     180     190     200
      VGCMLCSMDVRLPSPDCPFPRRVKLPKGKCEEWVCDEPKDQTVVG--PALAAYRLEDTFGPDPTMIRANCL
      :      :      :      :      :      :      :
TGTGACCTTTGGCTAGCCCTGGACTATGTGGTCAGCAATGCCTCAGTTATGAATCTGCTCATCAT--CAGC-
410 420 430 440 450 460 470

      210     220     230     240     250     260     270
      VQTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKG--KKCIRTPKISKPIKFEL
      :      :      :      :      :      :      :
-TTTGACAGGTACTTCTGT-GTCACAAAACCTCTGACCTACCCAGTCAAGCGGACCACAAAAATGGCAGGTA
480 490 500 510 520 530 540

      280     290     300     310     320     330
      SGCTSMKTYRAKFCGVCT-DGRCCTPHRTTTL PVEFKCPDGEVMKKNMMFIKTC---ACHYNCPGDNDIFES
      :      :      :      :      :      :
TGATGATTGCAGCTGCCTGGGTCCTCTCTTTTCATCCTCTGGGCTCCAGCCATTCTCTTCTGGCAGTTTCATTG
550 560 570 580 590 600 610

340 X
  LYYRKM YGDMA
      :
TAGGGGTGAGAACTGTGGAGG
620 X 630

```

2. US-07-752-427-2 (1-349)

P60053 Sequence of von Willebrand factor (vWF).

ID P60053 standard; Protein; 2813 AA.
 AC P60053;
 DT 22-JUL-1991 (first entry)
 DE Sequence of von Willebrand factor (vWF).
 KW Vascular injury; platelet plug formation.
 OS Homo sapiens.
 PN EP-197592-A.
 PD 15-OCT-1986.
 PF 26-MAR-1986; 200518.
 PR 01-APR-1985; NL-000961.

PH (VRIE-) STICHT VRIEND LANDS.
 PA (FRIN-) STICHT FRINDER RANT.
 PI Pannekoek H; Verwey O; Diergaarde PJ; Hart MHL;
 DR WPI; 86-273504/42.
 DR N-PSDB; N60061.
 PT Recombinant cDNA plasmid or phage - contg. C-DNA fragment which
 PT codes for biological activity of human von Willebrand factor
 PS Disclosure; Fig 3; 37pp; English.
 CC vWF (glyco) protein having the AA sequence corresponding to the
 CC nucleotide sequence of 2518-8667 or 295-2517 of N60061 is claimed.
 CC Also claimed are new microorganisms, animal cell or human cell contg.
 CC the recombinant cDNA plasmid or phage; e. g. strain E.coli DH1 contg.
 CC the recombinant cDNA plasmid pSP8800vWF is deposited as C. B. S. No
 CC 163. 86.
 SQ Sequence 2813 AA;
 SQ 160A; 137R; 101N; 160D; 0 B; 217C; 142Q; 181E; 0 Z; 207G; 77 H;
 SQ 97 I; 233L; 104K; 55 M; 93 F; 173P; 201S; 146T; 27 W; 81 Y; 221V;

Initial Score = 11 Optimized Score = 59 Significance = 4.54
 Residue Identity = 20% Matches = 77 Mismatches = 248
 Gaps = 43 Conservative Substitutions = 0

```

      X      10      20      30      40      50
      MTAASMG PVRV-AFVVLLALCSRPAVGQ-NC SGPC-RCPDEPAPRCPAGVSLVLDGCGCCRV
      |      |      |      |      |      |      |      |      |      |
NYNGNQGDDFLTPSGLAEPRVEDFGNAWKLGDCQDLQKQHS DPCALNPRMTRFSEEACAVLTSPTFEACHR
  530      X 540      550      560      570      580      590

60      70      80      90      100      110      120      130
CAKQLGELCTER-DPCDPHKGLFCDFGSPANRKIGVCTAKDGAPCIFGGTVYRSGESFQSSCKYQCTCLDGA
|      |      |      |      |      |      |      |      |      |
AVSPLPYLRNCRYDVCSCSDGRECLCGALA-----SYAACAGRGVRVAWREPGRCELNCPKQG-VYLQCG
  600      610      620      630      640      650      660

      140      150      160      170      180      190
VGCMLCSMDVRLPSPD-----CPFPRRVKLPKGKCEEWVCDEPKDQTVVGPALAAYRLEDTFGPD
|      |      |      |      |      |      |      |      |      |
TPCNLTC---RSLSYPD EECNEACLEGCFCP-----PGLYMDERGD CVPKAGCPCYYDGEIFQPEDIFSDHH
  670      680      690      700      710      720

      200      210      220      230      240      250      260
TMIRANCLVQTT EWSACSKTCGMGISTRVTNDNASCRLEKQS---RLCMV-RPCEADLEENIKKGKKCIRTP
||      |      |      |      |      |      |      |      |      |
TM---CYCEDGFMHCTMSGVPGSLLPDAVLSSPLSHR-SKRSLSCRPPMVKLVCPAD---NLRAEGLECTKT-
  730      740      750      760      770      780      790

      270      280      290      300      310      320      330
KISKPIKFELSGCTSMKTYRAKFCGVCTDGRCTPHRTTTL PVEFKCPDGEVMKKNNMMFIKTCACHYNC-PG
||      |      |      |      |      |      |      |      |      |
CQNYDLECM SMGCVS---GCLCPPGMVRHENRCVALERCPCFHQGKEYAPGETVKIGCNTCVCRDRKWNCTDH
  800      810      820      830      840      850      860

      340      X
DNDIFESLYRKMYGDMA
|      |      |
VCDATCSTIGMAHYLTFDGLKYLFPGEC
  870      880
  
```

3. US-07-752-427-2 (1-349)

P60462 Sequence of human von Willebrand Factor (VWF) prec

ID P60462 standard; Protein; 2813 AA.
 AC P60462;
 DT 25-JUN-1991 (first entry)
 DE Sequence of human von Willebrand Factor (VWF) precursor.

KW Chronic renal failure; therapy; factor VIII C.
 OS Homo sapiens.
 PN W08606096-A.
 PD 23-OCT-1986.
 PF 10-APR-1986; U00760.
 PR 11-APR-1985; US-722108.
 PA (CHIL-) CHILDRENS MED CENT.
 PA (GINS/) GINSBURG D.
 PI Ginsburg D, Orkin SH, Kaufman RJ;
 DR WPI; 86-291663/44.
 DR N-PSDB; N60404.
 PT Pure Von Willebrand Factor - produced using an expression vector
 PT including a DNA sequence encoding functional VWF protein
 PS Disclosure; Table 2, Pages 18-36A; 54pp; English.
 CC cDNA clones pVWH33, pVWH5 and PVWE6 which span 9 kb pairs of DNA and
 CC encompass the entire protein coding region of VWF, were selected to
 CC construct full length cDNA (N60404). The pure VWF produced is useful
 CC in the treatment of von Willebrand's disease (VWD) and the patients
 CC with chronic renal failure whose abnormal bleeding times are
 CC corrected by crude cryoprecipitate. Pure VWF can also be used to
 CC carry, stabilise and improve the therapeutic efficacy of factor
 CC VIII:C.
 SQ Sequence 2813 AA;
 SQ 154A; 143R; 98 N; 155D; 0 B; 234C; 133Q; 181E; 0 Z; 205G; 70 H;
 SQ 95 I; 227L; 108K; 56 M; 89 F; 176P; 207S; 151T; 26 W; 79 Y; 226V;

Initial Score = 7 Optimized Score = 59 Significance = 4.54
 Residue Identity = 20% Matches = 76 Mismatches = 259
 Gaps = 28 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      MTAASMG-PVRVAFVLLALCSRPAV-GQNCSGPCRCPPDEAPRCPPAGVSLVLDGCGCCRV
      :      :      :      :      :      :      :
CLPDKVCVHRSTIYPVGQFWEEGCDVCTCTDMEDAVMGLRVAQCSQKPCE--DSCRSGFTYVLHEGECCGR
2430      X 2440      2450      2460      2470      2480      2490

      70      80      90      100     110     120
      AKQLGELCT---ERDPCDPHKGLFCDFGSPAN-RKIGVCTAKDGAPCIFGGTV-YRSGESFQSSCKYQCTCL
      :      :      :      :      :      :      :
LPSACEVVTGSPRGDSQSSWKSQVGSQWASPENPCLINECVRVKEEVFIQQRNVSCPQLEVPVCPSPGFQLSCK
2500      2510      2520      2530      2540      2550      2560

      130     140     150     160     170     180     190
      DGAVGCMPLCSMDVRLPSPDCPFPRRVKLPQKCCSEWVCDEPKDQTVVGPALAAAYRLE---DTFGPDPTMIR
      :      :      :      :      :      :      :
TSA--CCPSC---RCERMEACMLNGTVIGPGKTVMIDVCTTCRCMVQVG-VISGFKLECRKTTCPNCP--LG
2570      2580      2590      2600      2610      2620      2630

      200     210     220     230     240     250     260
      ANCLVQTTWEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIIRTPKISKPIKF
      :      :      :      :      :      :      :
YKEENNTGECCGRCLPTACTIQLRGGQIMTLKRDETLQDGCDFHFC-KVNERGEYFWEKRVTGCPFFDEHKC
2640      2650      2660      2670      2680      2690      2700

      270     280     290     300     310     320     330
      ELSGCTSMKTYRAKFCGVCTDGRCTPHRTTTL-PVEFKCPDGEVMKKNNMFIKTCACHYNCPGD-ND--IF
      :      :      :      :      :      :      :
LAEGGKIMK-IPGTCCDTCEEPEC--NDITARLQYVKVGSKSEVEVDIHYCQKGCASKAMYSIDINDVQDQ
2710      2720      2730      2740      2750      2760      2770

      340      X
      ESLYYRKMYGDMA
      :      :
      CSCCSPTRTEPMQVALHCTNGSV
      2780      X      2790
  
```

4. US-07-752-427-2 (1-349)
P93284 Sequence of clone HIV-2 SBL/ISY.

ID P93284 standard; protein; 3025 AA.
AC P93284;
DT 06-APR-1990 (first entry)
DE Sequence of clone HIV-2 SBL/ISY.
KW HIV-2; proviral clone HIV-2 SBL/ISY;
OS Human immunodeficiency virus 2.
PN US7331212-A.
PD 29-AUG-1989.
PF 31-MAR-1989; 331212.
PR 31-MAR-1989; US-331212.
PA (USSH) US Dept. Health and Human Services.
PI Franchini G, Wong-Staal F, Gallo R;
DR WPI; 89-339698/46.
DR N-PSDB; N92119.
PT Complete human immunodeficiency type 2 proviral clone - used to generate
PT animal model for function studies of HIV genes in vivo.
PS Disclosure; Fig. 5; 43pp; English.
CC The protein is encoded by the second reading frame of HIV-2 SBL/ISY, a
CC proviral clone of HIV-2.
SQ Sequence 3025 AA;
SQ 143 A; 278 R; 126 N; 104 D; 0 B; 96 C; 191 Q; 115 E; 0 Z; 244 G;
SQ 95 H; 153 I; 224 L; 246 K; 65 M; 63 F; 160 P; 291 S; 193 T; 53 W;
SQ 80 Y; 105 V;

Initial Score = 15 Optimized Score = 57 Significance = 3.89
Residue Identity = 20% Matches = 75 Mismatches = 256
Gaps = 41 Conservative Substitutions = 0

```

      X      10      20      30      40      50
      MTAASMG PVRVAFV VLLALCS RPAVG QNC SGPCRC PDEPA-----PRCPAGVSLVLDGCGC
            |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
MDSHPETSGCPKLG GTNLPRNKD QTLMA--NRKDDTHGRSTVD RISR SRAGGK QNYLKP GTGGTLLPRGKRV
 980      990      1000      1010      1020      1030      1040

      60      70      80      90      100      110      120
CRVCAK----QLGELCTERDPCDP HKGLFCDFG SPANRKIGVCTAKDGAPC IFGGTVYRSGESF QSSCKYQCT
            |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
RSNSSKGSR QSVDISTPGRKNSKSRKICKDKKYPY QRG QVVG T----GSEN RKRSTSHLGTNTKISPTSRKR
1050      1060      1070      1080      1090      1100      1110

      130      140      150      160      170      180      190
CLDGAVGCMPLCS-MDVRLPSPDCPFPRRVKLP GKCC EEWVCDEPKD QTVVGPALAA-----YRLEDTFGPD
            |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DLGT VVG--LLASDMDPRLGLRIHPTV GQVSIPGKRSYTRRD-----LLHG WILQAIKRGKSR IYNRRKRQ
1120      1130      1140      1150      1160      1170      1180

      200      210      220      230      240      250
PTMIRANCLV QTT EWSACSKTCGMGISTRVTNDNASCR L-----EK QSR LCMVRPCEADLEENIKKG-KKCIR
            |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
SKDIRAN--YQPT--SRIRSLCNGSNRLRSKS QYCS-RLTV CNGNSNRPTGIRENSKNYRRDDKKG SNLCCM
      1190      1200      1210      1220      1230      1240

      260      270      280      290      300      310      320
TP-KISKPIKFELSGCTS-MKTYRAKFCGVCTDGR-CCTPHRTTTL PVEFKCPDGEVMKKNMFIKTCACHY
            |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
GPGPQRHRRKSRNPLSKSGHQTSIIPRENRRASGR TWKIS QCKRTSPVWIT QPGGKTNSKHMCPVPPTKRGSY
1250      1260      1270      1280      1290      1300      1310

      330      340      X
NCPGDNDIFESLYYRKMYGDMA
            |   |   |
-TWASKCRTRHLANGLHTLRMKNHYSSSTCK

```


270 280 290 300 310 320
K I S - K P I K F E L S G C T S M K T Y R A K P C G V C T D G R C C T P H R T T T L P V E F K C P D - - G E V M K K N M M F I K T C A C H Y N C


```

      10      20      30      40      50      60
MTAASMG PVRVAFV VLLALCSRPAVGQNC SGPCRC PDPA PRCPAGVSLVLDGCGCCRVCAK
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
KRTENVQYRHVELARVGQV-VEVD TLEHVQHI IGGAGNDSITGNAHD----NFLAGGSGDDRLDGGAGNDTL
      730 X      740      750      760      770      780

      70      80      90      100     110     120     130
QLGELCTERDPCDPHKGLFCDFGSPAN---RKIGVCTAKDGAPCIFGGTVYRSGESFQSSCKYQCTCLDGAV
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
VGGEGQNTVIGGAGDDVFLQDLGVWSNQLDGGAGVDTV KYNVHQ PSEERLERMG-----DTGIHADLQKGTV
790      800      810      820      830      840      850

      140     150     160     170     180     190
GCMP---LCSMDVRLPSPDCPFPR---RVKLP GKCC EEWVCDEPKDQTVVG--PALAAYRLED T-FGPDPTM
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
EKWPALNLFSDVHVKN IENLHGSRLNDRIAGDDQDNELWGH DGN D TIRGRGGDDILRGGLGLDTLYGEDGND
      860      870      880      890      900      910      920

      200     210     220     230     240     250     260
IRANCLVQTT EWSACSKTCGMGISTRVTNDNASCRLEKQSR LCMVRPCEADLEENIKKGKKCIRTPKISKPI
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
I-----FLQDDET VSD D IDGGAGLDT-VDYSAMIHPGRIVAPHEYGFGIEADLSREWVRKASALGVDYYDNVR
      930      940      950      960      970      980      990

      270     280     290     300     310     320     330
KFELSGCTSMK---TYRAKFCGVCTDGRCC TPHRTTTL PVEFKCPDGEVMKKNNMMFIKTCACHYNCPGDNDI
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NVENVIGTSMKDV LIGDAQANTLMGQGGDDT-VRGGDGD D L LFGGDGNDMLYGDAGNDT---LYGGLGD-DT
      1000     1010     1020     1030     1040     1050     1060

      340      X
FESLYYRKMYGDMA
      :  :
LEGGAGNDWFGQTQAREH D VLRGG
      1070      X 1080
```

9. US-07-752-427-2 (1-349)

R08267 Platelet derived growth factor (PDGF) receptor pro

ID R08267 standard; protein; 1089 AA.
AC R08267;
DT 07-MAR-1991 (first entry)
DE Platelet derived growth factor (PDGF) receptor protein.
KW Atherosclerosis; fibrotic diseases.
OS Homo sapiens.
PN W09014425-A.
PD 29-NOV-1990.
PF 21-MAY-1990; U02849.
PR 22-MAY-1989; US-355018.
PA (ZYMO-) ZYMOGENETICS INC.
PI Kelly JD, Murray MJ;
DR WPI; 90-375992/50.
DR N-PSDB; Q06869.
PT DNA encoding platelet-derived growth factor - used to transform
PT cells for culturing to detect PDG agonists and antagonists
PS Claim 1; Fig 1; 30pp; English.
CC Gene product may be expressed from a transformed cell. It has
CC utility in dection of PDGF agonist and antagonist analogues, binding
CC AA, AB and BB isoforms. PDGF agonists may be used to enhance wound
CC healing, and antagonists may be used to block the effects of PDGF
CC eg. in treatment of atherosclerosis or fibrotic diseases.
SQ Sequence 1089 AA;
SQ 54 A; 44 R; 44 N; 66 D; 0 B; 17 C; 25 Q; 94 E; 0 Z; 58 G; 25 H;

SW 71 I; 105L; 69 K; 25 M; 32 F; 51 P; 93 S; 68 T; 13 W; 47 Y; 88 V;

Initial Score = 6 Optimized Score = 56 Significance = 3.57
Residue Identity = 19% Matches = 72 Mismatches = 251
Gaps = 44 Conservative Substitutions = 0

```

      X   10           20           30           40           50           60
MTAASMGFVRVAFVVL-LALCSRPAVGQNCSGPCRCPDPAAPRCAGVSLVLDGCGCCRV-----CAKQLGEL
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESS
      X   10           20           30           40           50           60

      70           80           90          100          110          120          130
CTERDPCDPHKGLFCDFGSPANRKIGVCTAKDGAPCIFGGTVY-----RSGESFQSSCKYQCTCLDGAVGCMF
  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DVEIRNEENNSSLF-----VTLLLEVSSA--SAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFFVP
      70           80           90          100          110          120          130

      140          150          160          170          180          190
LCSMDVRLPSPD---CPFFRRVKLPKGCCEEWVCDEPKDQTVVGPAALAYR---LEDTFGPDPTMIRA---NC
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
LGMTDYLVLIVEDDDSAIIPCRITDP---ETPV--TLHNSEGVVPASYDSRQGFNGTFTVGPYICEATVKGK
      140          150          160          170          180          190

200          210          220          230          240          250          260
LVQT--TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPIKFE
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
KFQTIFFNVYALKAT-----SELDLEMEALKTVYK-SGETIVVTCVAFNNEVVDLQWTYPGEVKGKGITILE
      200          210          220          230          240          250          260

270          280          290          300          310          320          330
LSGCTSMK---TYRAKFCGVCTDGRCTPHRTTTLTPV-EFKCPDGEVMKKNNMFIKTCACHYNCPGDNDIFE
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
EIKVPSIKLVYTLTVPEATVKDSGDYECARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKH
      270          280          290          300          310          320          330

340          X
SLYYRKMYGDMA
  |
FVVEVRAYPPPRISWLKNNLTL
      340          X 350
```

10. US-07-752-427-2 (1-349)

R06910 Alpha type PDGF receptor deduced from TR4 cDNA clo

ID R06910 standard; protein; 1089 AA.
AC R06910;
DT 16-JAN-1991 (first entry)
DE Alpha type PDGF receptor deduced from TR4 cDNA clone.
KW Platelet derived growth factor; T11.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 1..23
FT /label=signal peptide
FT Domain 24..524
FT /label=ligand binding domain
FT Domain 525..548
FT /label=transmembrane region
FT Domain 549..599
FT /label=juxtamembrane domain
FT Binding-site 600..627
FT /label=ATP binding site
FT Modified-site 849
FT /label=tyrosine autophosphorylation site
FT Modified-site 42..44

